SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: de la Torre, Juan C.

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING OF HUMAN BORNA DISEASE VIRUS

(iii) NUMBER OF SEQUENCES: 65

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
(B) STREET: 10550 North Torrey Pines Road, TPC-8
(C) CITY: La Jolla
(D) STATE: California
(E) COUNTRY: United States
(F) ZIP: 92037

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE: 7-JAN-1997
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Fitting, Thomas
(B) REGISTRATION NUMBER: 34,163
(C) REFERENCE/DOCKET NUMBER: TSRI 465.0

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (619) 784-2937
(B) TELEFAX: (619) 784-9399

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8910 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTTGCGTTAA CAACAAACCA MTCATYATYC TTCTAACAAA ATGAACACAC GCAATGCCAC 60

CCAAGAGACG CCTGGTTGAT GACGCCGATG CCATGGAGGA YCAAGATYTA TATGAACCCC 120

CAGCGAGCCT CCCYAAGCTC CCYGGRAAAT TCCTACAATA CACCGTTGGG GGGTCTGACC 180

CGCATCCGGG TATAGGGCAT GAGAARGAYA TCAGGCAGAA CGCAGTGGCA TTGTTAGACC 240

AGTCACGGCG CGATATGTTT CAYACAGTAA CGCCYAGCCT TGTGTTTCTA TGTTTGCTAA 300

TCCCAGGACT GCACGCTGCG TTTGTTCACG GAGGGGTGCC TCGTGAATCY TACCTGTCGA 360

CGCCTGTYAC GCGTGGRGAA CAGACTGTYG TTAAGACTGC RAAGTTTTAC GGGGAAAAGA 420

CRACRCAGCG TGATCTCACC GAGCTGGAGA TCTCCTCTAT MTTCAGCCAT TGTTGCTCAT 480

TACTAATWGG GGTTGTGATA GGATCGTCRT CTAAGATYAA AGCAGGAGCC GAGCAGATCA 540

AGAAAAGGTT TAAAACTATG ATGGCAGCCT TAAACCGGCC ATCCCATGGT GAGACTGCTA 600

CACTACTYCA GATGTTTAAT CCACATGAGG CTATAGATTG GATTAACGGC CARCCCTGGG 660

TAGGCTCCTT TGTGTTGTCT CTACTAACTA CAGACTTTGA GTCCCCAGGT AAAGAATTYA 720

TGGAYCAGAT TAARCTTGTC GCAAGTTATG CRCAGATGAC TACGTACACT ACTATAAAGG 780

AGTACCTCGC AGAATGYATG GATGCTACCC TTACAATCCC YGTAGTTGCA TATGAGATYC 840

GTGACTTTTT AGAAGTTTCA GCAAAGCTTA ARGAGGAWCA TGCTGACCTG TTYCCGTTYC 900

TGGGGGCYAT TMGRCACCCC GACGCTATCA AGCTKGCGCC ACGRAGCTTT CCCAATCTGG 960

CYTCYGCAGC GTTTTACTGG AGTAAGAAGG ARAAYCCCAC AATGGCRGGC TACCGGGCCT 1020

CCACCATCCA GCCGGGCGCR AGTGTCAAGG ARACCCAGCT TGCCCGGTAT AGGCGCCGCG 1080

AGATATCTCG YGGRGARGAC GGGGCAGAGC TCTCAGGTGA GATCTCTGCC ATAATGARRA 1140

TGATAGGTGT GACTGGTCTA AACTARAAAA CAATGAACAA ACCAATAAAA AACCAAATGC 1200

GGCAAACCCY CCGCGACCTG YGATGAGYTC CGACCTCCGG CTGACATTGC TTGAAYTAGT 1260

CAGGAGGCTC AATGGCAACG SGACCATCGA GTCTGGTCGA CTCCCTGGAG GACGAAGAAG 1320

ATCCCCAGAC ACTACGACGG GAACGAYCGG GGTCACCAAG ACCACGGAAG RTCCCAAGGA 1380

ATGCATTGAC CCAACCRGTA GACCAGCTCC TGAAGGACCT CAGGAAGAAC CCCTCCATGA 1440

TCTCAGACCC AGACCAGCGA ACCGGAAGGG AGCAGCTRTC GAATGATGAG CTWATCAAGA 1500

AGYTAGTGAC GGAGCTGGCC GAGAATAGCA TGATCGAGGC TGAGGAGGTG CGGGGCACTC 1560

TTGGRGACAT CTCGGCTCGY ATCGAGGCAG GGTTTGAGTC CCTGTCCGCC CTCCAAGTGG 1620

AAACCATCCA GACAGCTCAG CGGTGCGAYC ACTCCGAYAG CATCAGRATC CTYGGCGAGA 1680

ACATCAAGAT ACTRGATCGC TCCATGAAGA CAATGATGGA GACAATGAAG CTCATGATGG 1740

AGAAGGTGGA YCTCCTCTAC GCATCAACCG CCGTTGGGAC CTCTGCACCC ATGTTGCCCT 1800

CCCATCCTGC ACCTCCGCGC ATTTATCCCC AGCTCCCAAG TGCCCCGACA RCGGATGART 1860

GGGACATCAT ACCATAAAAA AATCGAATCA CCATGAATTC AAARCATTCC TATGTGGAGC 1920

TCAAGGRCAA GGTAATCGTC CCTGGATGGC CCACACTGAT GCTTGAGATA GACTTTGTAG 1980

GRGGGACTTC ACGGAACCAG TTCCTTAACA TCCCATTTCT TTCAGTGAAA GAGCCTCTGC 2040

AGCTTCCACG CGAGAAGAAG TTGACCGACT ACTTYACYAT TGACGTAGAR CCAGCAGGTC 2100

ATTCCCTGGT CAAYATATAC TTCCAGATTG ACGACTTCTT GCTCCTAACA CTCAACTCAC 2160

TRTCYGTRTA CAAGGACCCG ATTAGRAAAT ACATGTTCCT ACGCCTCAAC AAGGAMCAGA 2220

GCAAGCACGC AATYAATGCA GCYTTCAATG TCTTYTCTTA TCGGCTTCGG AACATTGGTG 2280

TTGGYCCTCT CGGCCCRGAC ATTCGATCTT CAGGGCCTTA GYTGCAATAC TGACTCCACT 2340

CCTGGAYTRA TYGAYCTGGA GATAAGGCGA CTTTGCCACA CCCCAACGGA AAATGTCATT 2400

TCATGCGAGG TTAGTTATCT YAACCACACG ACTATTAGCC TCCCGGCAGT CCACACRTCA 2460

TGCCTCAAGT ACCACTGCAA AACCTATTGG GGATTCTTTG GTAGCTACAG CGCTGACCGA 2520

ATCATMAATC GGTACACTGG TACTGTTAAG GGTTGTYTAA ACAACTCAGC RCCAGAGGAY 2580

CCCTTCGAGT GCAACTGGTT CTACTGCTGC TCGGCGATTA CAACAGAGAT CTGCCGATGC 2640

TCTATTACAA ATGTCACGGT GGCTGTRCAR ACATTCCCAC CGTTCATGTA CTGCAGTTTY 2700

GCRGACTGYA GTACYGTGAG YCARCAGGAG CTAGAGAGTG GMAAGGCAAT GCTGAGCGAT 2760

GGCAGTACMT TAACTTATAC CCCGTATATC YTACARTCAG AAGTCGTGAA CAAAACCCTY 2820

AATGGGACYA TACTCTGCAA CTCATCCTCY AAGATAGTTT CCTTCGATGA ATTTAGGCGT 2880

TCATACTCCC TARCGAATGG TAGTTACCAG AGCTCATCAA TCAATGTGAC GTGTGYAAAC 2940

TACACGTCGT CCTGCCGGYC CARGTTGARA AGGCGGCGTA GGGAYACYCA RCAGATTGAG 3000

TAYCTAGTTC ACAAGCTTAG GCCYACACTG AAAGATGCRT GGGAGGACTG TGAGATCCTC 3060

CAGTCTCTGC TCCTAGGGRT GTTTGGTACT GGGATYGCAA GTGCTTCKCA ATTYTTGAGG 3120

RGCTGGCTCA ACCACCCTGA YATCATCGGG TATATAGTTA ATGGAGTTGG GGTWGTCTGG 3180

CAATGCCATC GTGTTAATGT CACGTTCATG GCGTGGAATG AGTCCACMTA TTACCCTCCA 3240

GTAGATTACA ATGGRCGGAA GTACTTYCTG AATGATGAGG GRAGGYTACA AACAAACACC 3300

CCCGAGGCAA GGCCAGGGCT TAAGCGGGTC ATGTGGTTCG GCAGGTACTT CCTAGGGACA 3360

GTAGGGTCTG GGGTGAAACC GAGGAGGATT CGGTACAATA AGACCTCACA TGAYTACCAY 3420

CTRGAGGAGT TTGAGGCAAG TCTCAACATG ACCCCYCAGA CCAGTATCGC CTCGGGTCAT 3480

GAGACAGACC CCATAAATCA TGCCTACGGA ACGCAGGCTG AYCTCCTTCC ATACACCAGG 3540

TCTAGTAATA TAAGRTCTAC RGATACAGGC TCAGGCTGGG TGCACATCGG CCTACCCTCA 3600

TTTGCTTTCC TCAATCCYCT CGGGTGGCTY AGGGACCTAC TTGCRTGGGC RGCCTGGTTG 3660

GGTGGGGTTC TATACTTAAT AAGTCTTTGT GTTTCCTTAC CAGCCTCCTT CGCGAGGAGG 3720

AGACGCCTCG GCCGGTGGCA GGAATAAACC GTACCGACCA RWCTCTTAAA AACCCTCTYC 3780

TCGGRACAGA GGTCTCTTTC TGCCTTAART CGAGYTCACT CCCCCATCAY GTACGAGCAY 3840

TRGGCCAGAT TAAAGCAARG AACCTGGCAT CCTGTGACTA TTACTTGCTA TTCCGCCAAG 3900

TTGTATTGCC CCCTGAAGTA TATCCCATTG GTGTYYTAAT AAGAGCTGCG GAGGCYATAC 3960

TAACAGTTAT AGTATCAGCT TGGAAGCTGG ATCAYATGAC RAAGACCCTA TACTCCTCTG 4020

TGAGATATGC ACTCACCAAT CCCCGGGTCC GRGCCCAACT TGAGCTYCAC ATTGCCTACC 4080

AGCGCATAGT GGGTCAGGTC TCGTAYAGCC GGGARGCAGA YATAGGGCCA AAAAGGCTTG 4140

GGAATATGTC ATTGCAATTC ATCCAATCYC TCGTTATTGC CACCATAGAC ACRACRAGCT 4200

GCCTAATGAC CTACAACCAC TTTCTTGCTG CAGCAGACAC AGCCAAGAGC AGATGCCAYC 4260

TCCTAATCGC CTCAGTGGTC CARGGRGCCC TTTGGGARCA AGGGTCATTT CTTGATCATA 4320

TAATCAACAT GATCGACAYA ATTGACTCAA TCAACCTCCC CCATGATGAT TACTTCACAA 4380

TTATTAAGTC TATCTYTCCC TACTCCCAAG GGCTTGTTAT GGGGAGGCAY AATGTRTCAG 4440

TCTCCTCTGA TTTYGCGTCC GTATTTRCYA TTCCTGAATY ATGCCCRCAA CTAGACAGCT 4500

TACTAAAAAA ACTGCTYCAA CTTGACCCYG TTCTCCTCCT CATGGTCTCT TCGGTGCAGA 4560

AGTCATGGTA CTTCCCTGAG ATCCGAATGG TYGACGGGTC ACGGGAGCAG CTCCACAAGA 4620

TGCGTGTCGA GCTGGARACG CCCCAAGCCC TGCTGTCRTA CGGCCATACC CTCCTGTCAA 4680

TATTTCGRGC AGAGTTTATC AAAGGCTATG TCTCAAAGAA TGCGAAGTGG CCGCCYGTAC 4740

ACCTGCTCCC AGGCTGTGAC AAATCCATAA ARAATGCGAG AGAGCTGGGC CGCTGGAGCC 4800

CGGYRTTTGA CCGACGATGG CAGCTCTTCG MGAAGGTTGT CATTCTAAGA ATTGCTGACC 4860

TAGATATGGA TCCCGACTTC AACGATATTG TTAGCGAYAA GGCGATAATC AGCTCAAGAA 4920

GGGACTGGGT ATTYGAGTAC AATGCAGCRG CCTTTTGGAA GAAATACRGT GARCGGTTGG 4980

AGAGGCCYCC TGCCAGRTCG GGACCRTCAC GRCTTGTGAA TGCTCTRATC GATGGACGCT 5040

TAGAYAATAT CCCAGCCCTG CTAGAGCCAT TTTACAGGGG AGCGGTTGAG TTYGAGGATC 5100

GGYTGACTGT GCTCGTGCCT AAGGAGAARG AGTTRAAGGT AAAGGGAAGG TTCTTCTCGA 5160

AGCAAACATT GGCAATCAGG ATATATCAGG TTGTTGCTGA AGCTGCACTT AAGAAYGAGG 5220

TTATGCCATA CYTAAARACA CAYTCAATGA CCATGAGCTC AACGGCYCTA ACYCAYCTTC 5280

TTAACCGGCT ATCACATACT ATCACTAAGG GTGACTCCTT TGTTATTAAC YTWGAYTATA 5340

GYTCCTGGTG CAACGGTTTC CGACCAGAAC TRCARGCCCC AMTCTGTCGT CAGTTGGATC 5400

AGATGTTCAA TTGCGGGTAC TTCTTCAGGA CTGGGTGCAC ACTGCCATGC TTTACCACGT 5460

TTATTATTCA RGACAGRTTC AACCCGCCCT ATTCCYTCMG TGGTGAGCCC GTTGAAGACG 5520

GWGTYACATG CGCGGTTGGG ACTAARACAA TGGGRGAGGG YATGAGGCAG AAACTATGGA 5580

CAATYCTTAC GAGCTGCTGG GAGATAATTG CTCTTCGGGA AATTAACGTG ACGTTTAAYA 5640

TACTAGGCCA RGGTGATAAT CAGACAATCA TYRTACATAA ATCTGCAAGC CAAAATAAYC 5700

AGCTATTAGC GGAGCGAGCA YTRGGRGCYY TGTACAAGCA TGCTAGATTA GCTGGCCATA 5760

ACCTYAAGGT AGARGAATGY TGGGTGTCAG ATTGTCTGTA TGAGTATGGA AAGAAGCTYT 5820

TCTTCCGTGG TGTACCTGTC CCRGGCTGTT TGAAGCAGCT CTCRCGGGTG ACGGAYTCYA 5880

CTGGRGAGYT ATTCCCAAAC CTATACTCAA AGTTAGCCTG CTTAACATCA TCRTGYTTAA 5940

GCGCAGCGAT GGCAGACACA TCYCCATGGG TGGCACTCGC GACAGGTGTC TGTCTGTATC 6000

TTATCGAGTT RTATGTTGAG CTGCCTCCRG CAATCATGCA GGAYGAGTCG CTRTTRACGA 6060

CCCTCTGYCT CGTAGGYCCA TCCATTGGTG GGCTTCCRAC YCCTGCAACC CTRCCCAGTG 6120

TCTTTTTCAG AGGAATGTCC GACCCAYTGC CCTTTCAGCT AGCACTCTTG CAGACCCTCA 6180

TTAARACGAC AGGGGTGACY TGTAGCTTGG TGAATCGTGT GGTYAAGTTA CGGATAGCAC 6240

CCTATCCAGA CTGGCTCTCY CTAGTGACTG ACCCGACYTC ACTCAACATT GCYCARGTGT 6300

ACCGGCCAGA ACGTCARATC AGGAGGTGGA TTGAGGARGC RATAGCRACA AGCTCACACT 6360

CGTCACGCAT AGCAACTTTY TTCCAGCAGS CCCTCACGGA GATGGCYCAG YTGCTTGCGA 6420

GGGACCTYTC AACAATGATG CCTCTTCGRC CCCGGGATAT GTCGGCCTTA TTCGCATTAT 6480

CAAATGTCGC ATAYGGTYTA AGCATTATAG ATCTATTTCA AAARTCCTCT ACCGTTGTYT 6540

CTGCAAGTCA AGCTGTCCAT ATCGARGATG TTGCCCTAGA GAGTGTAAGG TATAAGGAAT 6600

CTATCATYCA GGGTCTGTTA GACACYACTG AGGGGTAYAA CATGCAACCT TATTTGGAAG 6660

GTTGCACTTA CCTTGCAGCC AARCAGYTAC GKAGGTTGAC RTGGGGTCGA GACCTAGTTG 6720

GAGTYACAAT GCCGTTTGTT GCCGAGCAAT TCCATCCYCA YAGTTCTGTS GGTGCAAARG 6780

CRGAACTCTA CCTCGAYGCT ATYATATACT GCCCACARGA GACRTTGCGG TCACACCATC 6840

TGACTACCAG GGGGGACCAG CCGCTTTACC TYGGATCYAA TACGGCTGTC AMGGTYCAGC 6900

GAGGTGAGAT CACRGGCCTA ACAAAGTCAA GGGCTGCAAA TCTAGTCARG GACACTCTCG 6960

TTCTCCAYCA GTGGTAYAAR GTCCGTAARG TTACCGATCC ACACTTGAAC ACYCTCATGG 7020

CRCGCTTCTT RCTTGAGAAG GGRTACACAT CTGACGCTCG RCCTAGCATY CAGGGTGGGA 7080

CCCTCACRCA TCGTCTCCCA TCCCGYGGAG ACTCACGSCA RGGGCTYACT GGGTATGTRA 7140

ATATACTMAG YACGTGGCTY CGRTTCTCAA GTGATTATCT TCACTCTTTC TCGAAATCAT 7200

CAGAYGACTA YACAATCCAC TTYCAGCATG TATTCACATA CGGTTGCCTC TATGCTGATT 7260

CGGTGATTAG ATCGGGCGGT GTTATTTCCA CTCCTTACCT TTTGAGTGCA AGTTGTAAAA 7320

CATGCTTTGA GAAGATAGAC TCAGAGGAGK TCGTCCTGGC ATGYGAACCY CAATAYAGGG 7380

GTGCTGAGTG GCTGATATCA AAGCCAGTYA CTGTCCCTGA GCAGATAAYT GAYGCTGAAG 7440

TCGAGTTTGA CCCCTGTGTG AGTGCGRGTT ATTGTCTCGG GATTCTCATT GGCAAGTCAT 7500

TCTTRGTTGA CATAAGGGCA AGTGGGCATG ATATYATGGA GCAGCGGACA TGGGCTAACY 7560

TGGAGAGGTT TTCTGTRTCG GACATGCAGA AACTTCCRTG GAGTATTGTA ATTCGGTCTC 7620

TCTGGAGATT CCTTATTGGC GCACGRCTCC TYCAGTTTGA GAAGGCTGGC CTYATTAGRA 7680

TGCTGTATGC TGCRACAGGT CCAACCYYTA GCTTCCTAAT GAAAGTYTTT CAAGACTCAG 7740

CCCTMCTYAT GGACTGCGCA CCYCTYGATC GGCTGTMCCC TAGGATCAAC TTTCATAGTC 7800

GGGGAGACCT CGTYGCYAAG CTYGTTTTAT TRCCCTTCAT CAACCCGGGT ATAGTGGAGA 7860

TTGAAGTGTC TRGAATTAAT AGCAAGTAYC ATGCAGTATC GGAGGCYAAT ATGGATCTGT 7920

ACATCGCTGC TGCMAARTCT GTGGGCGTRA AGCCCACACA GTTTGTTGAG GAAACAAACG 7980

ACTTTACGGC CCGCGGCCAC CACCATGGTT GTTATTCCCT TTCTTGGTCT AAGTCACGCA 8040

ATCAATCACA GGTCCTAAAG ATGGTAGTRC GGAAGCTGAA GCTMTGTGTC CTGTATATAT 8100

ACCCCACAGT CGATCCCGCC GTTGCTCTCG ACCTGTGCCA YCTRCCAGCA YTAACTATAA 8160

TCCTAGTGCT CGGCGGTGAC CCAGCGTACT AYGAGCGATT ACTTGAGATG GACCTRTGCG 8220

GGGCTGTGTC AAGTCGMGTY GATATCCCCC ATTCYCTRGC TGSCAGAACG CACAGGGGGT 8280

TCRCARTRGG CCCAGACGCT GGTCCAGGTG TRATTAGACT YGACARGTTA GAGTCRGTTT 8340

GTTAYGCYCA CCCCTGTTTR GAGGARCTAG AGTTTAATGC RTAYCTAGAC TCTGAGTTRG 8400

TTGAYATTAG TGATATGTGC TGCCTCCCCY TAGCGACACC CTGTAAGGCC CTWTTCAGGC 8460

CARTRTATCG GAGCTTACAG TCGTTCAGGT TAGCCTTAAT GGACAACTAT AGTTTTGTMA 8520

TGGACCTCAT TAYGATCCGR GGRSTGGACA TYAGGCCTCA CCTTGAGGAR TTTGAYGARC 8580

TGCTTGTGGT RGGRCAGCAY ATCCTCGGYC AGCCCGTCCT AGTRGAGGTT GTTTACTACG 8640

TTGGAGTTGT TRGGAAGCGY CCTGTGTTAG CGAGGCATCC STGGTCAGCA GATCTTAAGC 8700

GAATYACTGT RGGGGGGCGR GCKCCCTGCC CYTCTGCTGC YRGAYTGCGT GATGAGGATT 8760

GTCRGGGGTC TCTGYTGGTT GGGCTTCCYG CTGGRTTGAC GCAGTTRTTG RTRRTTGATT 8820

RAGRTYRAGC CAYCTACTRC CCTATTCTTA AAAAACCATA YGTCAGTGGT GCAGTGCTTG 8880

GGYTTGGTTG TTGCTTTGTT GTAGCGCKTT 8910

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 603 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCAACGC GACCATCGAG TCTGGTCGAC TCCCTGGAGG ACGAAGAAGA TCCCCAGACA 60

CTACGACGGG AACGACCGGG GTCACCAAGA CCACGGAAGG TCCCAAGGAA TGCATTGACC 120

CAACCAGTAG ACCAGCTCCT GAAGGACCTC AGGAAGAACC CCTCCATGAT CTCAGACCCA 180

GACCAGCGAA CCGGAAGGGA GCAGCTGTCG AATGATGAGC TAATCAAGAA GTTAGTGACG 240

GAGCTGGCCG AGAATAGCAT GATCGAGGCT GAGGAGGTGC GGGGCACTCT TGGAGACATC 300

TCGGCTCGTA TCGAGGCAGG GTTTGAGTCC CTGTCCGCCC TCCAAGTGGA AACCATCCAG 360

ACAGCTCAGC GGTGCGATCA CTCCGACAGC ATCAGGATCC TCGGCGAGAA CATCAAGATA 420

CTAGATCGCT CCATGAAGAC AATGATGGAG ACAATGAAGC TCATGATGGA GAAGGTGGAT 480

CTCCTCTACG CATCAACCGC CGTTGGGACC TCTGCACCCA TGTTGCCCTC CCATCCTGCA 540

CCTCCGCGCA TTTATCCCCA GCTCCCAAGT GCCCCGACAA CGGATGAATG GGACATCATA 600

CCA 603

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 603 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGCAACGG AACCATCGAG TCTGGTCGAC TCCCTGGAGG ACGAAGAAGA TCCCCAGACA 60

CTACGACGGG AACGATCGGG GTCACCAAGA CCACGGAAGG TCCCAAGGAA TGCATTGACC 120

CAACCAGTAG ACCAGCTCCT GAAGGACCTC AGGAAGAACC CCTCCATGAT CTCAGACCCA 180

GACCAGCGAA CCGGAAGGGA GCAGCTGTCG AATGATGAGC TAATCAAGAA GTTAGTGACG 240

GAGCTGGCCG AGAATAGCAT GATCGAGGCT GAGGAGGTGC GGGGCACTCT TGGAGACATC 300

TCGGCTCGTA TCGAGGCAGG GTTTGAGTCC CTGTCCGCCC TCCAAGTGGA AACCATCCAG 360

ACAGCTCAGC GGTGCGATTA CTCCGACAGC ATCAGGATCC TCGGCGAGAA CATCAAGATA 420

CTAGATCGCT CCATGAAGAC AATGATGGAG ACAATGAAGC TCATGATGGA GAAGGTGGAT 480

CTCCTCTACG CATCAACCGC CGTTGGGACC TCTGCACCCA TGTTGCCCTC CCATCCTGCA 540

CCTCCGCGCA TTTATCCCCA GCTCCCAAGT GCCCCGACAA CGGATGAGTG GGACATCATA 600

CCA 603

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 603 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGGCAACGG GACCATCGAG TCTGGTCGAC TCCCTGGAGG ACGAAGAAGA TCCCCAGACA 60

CTACGACGGG AACGATCGGG GTCACCAAGA CCACGGAAGG TCCCAAGGAA TGCATTGACC 120

CAACCAGTAG ACCAGCTCCT GAAGGACCTC AGGAAGAACC CCTCCATGAT CTCAGACCCA 180

GACCAGCGAA CCGGAAGGGA GCAGCTGTCG AATGATGAGC TAATCAAGAA GTTAGTGACG 240

GAGCTGGCCG AGAATAGCAT GATCGAGGCT GAGGAGGTGC GGGGCACTCT TGGAGACATC 300

TCGGCTCGTA TCGAGGCAGG GTTTGAGTCC CTGTCCGCCC TCCAAGTGGA AACCATCCAG 360

ACAGCTCAGC GGTGCGATCA CTCCGACAGC ATCAGGATCC TCGGCGAGAA CATCAAGATA 420

CTAGATCGCT CCATGAAGAC AATGATGGAG ACAATGAAGC TCATGATGGA GAAGGTGGAT 480

CTCCTCTACG CATCAACCGC CGTTGGGACC TCTGCACCCA TGTTGCCCTC CCATCCTGCA 540

CCTCCGCGCA TTTATCCCCA GCTCCCAAGT GCCCCGACAA CGGATGAGTG GGACATCATA 600

CCA 603

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 603 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCAACGG AACCATCGAG TCTGGTCGAC TCCCTGGAGG ACGAAGAAGA TCCCCAGACA 60

CTACGACGGG AACGATCGGG GTCACCAAGA CCACGGAAGG TCCCAAGGAA TGCATTGACC 120

CAACCAGTAG ACCAGCTCCT GAAGGACCTC AGGAAGAACC CCTCCATGAT CTCAGACCCA 180

GACCAGCGAA CCGGAAGGGA GCAGCTGTCG AATGATGAGC TAATCAAGAA GTTAGTGACG 240

GAGCTGGCCG AGAATAGCAT GATCGAGGCT GAGGAGGTGC GGGGCACTCT TGGAGACATC 300

TCGGCTCGTA TCGAGGCAGG GTTTGAGTCC CTGTCCGCCC TCCAAGTGGA AACCATCCAG 360

ACAGCTCAGC GGTGCGACCA CTCCGACAGC ATCAGGATCC TCGGCGAGAA CATCAAGATA 420

CTAGATCGCT CCATGAAGAC AATGATGGAG ACAATGAAGC TCATGATGGA GAAGGTGGAT 480

CTCCTCTACG CATCAACCGC CGTTGGGACC TCTGCACCCA TGTTGCCCTC CCATCCTGCA 540

CCTCCGCGCA TTTATCCCCA GCTCCCAAGT GCCCCGACAA CGGATGAGTG GGACATCATA 600

CCA 603

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGAATTCAA AACATTCCTA TGTGGAGCTC AAGGACAAGG TAATCGTCCC TGGATGGCCC 60

ACACTGATGC TTGAGATAGA CTTTGTAGGG GGGACTTCAC GGAACCAGTT CCTTAACATC 120

CCATTTCTTT CAGTGAAAGA GCCTCTGCAG CTTCCACGCG AGAAGAAGTT GACCGACTAC 180

TTTACTATTG ACGTAGAACC AGCAGGTCAT TCCCTGGTCA ATATATACTT CCAGATTGAC 240

GACTTCTTGC TCCTAACACT CAACTCACTA TCTGTGTACA AGGACCCGAT TAGAAAATAC 300

ATGTTCCTAC GCCTCAACAA GGACCAGAGC AAGCACGCAA TCAATGCAGC CTTCAATGTC 360

TTTTCTTATC GGCTTCGGAA CATTGGTGTT GGTCCTCTCG GCCCGGACAT TCGATCTTCA 420

GGGCCT 426

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAATTCAA AGCATTCCTA TGTGGAGCTC AAGGACAAGG TAATCGTCCC TGGATGGCCC 60

ACACTGATGC TTGAGATAGA CTTTGTAGGG GGGACTTCAC GGAACCAGTT CCTTAACATC 120

CCATTTCTTT CAGTGAAAGA GCCTCTGCAG CTTCCACGCG AGAAGAAGTT GACCGACTAC 180

TTTACTATTG ACGTAGAACC AGCAGGTCAT TCCCTGGTCA ATATATACTT TCAGATTGAC 240

GACTTCTTGC TCCTAACACT CAACTCACTA TCTGTGTACA AGGACCCGAT TAGAAAATAC 300

ATGTTCCTAC GCCTCAACAA GGACCAGAGC AAGCACGCAA TCAATGCAGC CTTCAATGTC 360

TTTTCTTATC GGCTTCGGAA CATTGGTGTT GGTCCTCTCG GCCCGGACAT TCGATCTTCA 420

GGGCCT 426

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAATTCAA AGCATTCCTA TGTGGAGCTC AAGGACAAGG TAATCGTCCC TGGATGGCCC 60

ACACTGATGC TTGAGATAGA CTTTGTAGGG GGGACTTCAC GGAACCAGTT CCTTAACATC 120

CCATTTCTTT CAGTGAAAGA GCCTCTGCAG CTTCCACGCG AGAAGAAGTT GACCGACTAC 180

TTTACTATTG ACGTAGAACC AGCAGGTCAT TCCCTGGTCA ATATATACTT CCAGATTGAC 240

GACTTCTTGC TCCTAACACT CAACTCACTA TCTGTGTACA AGGACCCGAT TAGAAAATAC 300

ATGTTCCTAC GCCTCAACAA GGACCAGAGC AAGCACGCAA TCAATGCAGC CTTCAATGTC 360

TTTTCTTATC GGCTTCGGAA CATTGGTGTT GGTCCTCTCG GCCCGGACAT TCGATCTTCA 420

GGGCCT 426

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAATTCAA AGCATTCCTA TGTGGAGCTC AAGGACAAGG TAATCGTCCC TGGATGGCCC 60

ACACTGATGC TTGAGATAGG CTTTGTAGGG GGGACTTCAC GGAACCAGTT CCTTAACATC 120

CCATTTCTTT CAGTGAAAGA GCCTCTGCAG CTTCCACGCG AGAAGAAGTT GACCGACTAC 180

TTTACTATTG ACGTAGAACC AGCAGGTCAT TCCCTGGTCA ATATATACTT CCAGATTGAC 240

GACTTCTTGC TCCTAACACT CAACTCACTA TCTGTGTACA AGGACCCGAT TAGAAAATAC 300

ATGTTCCTAC GCCTCAACAA GGACCAGAGC AAGCACGCAA TCAATGCAGC CTTCAATGTC 360

TTTTCTTATC GGCTTCGGAA CATTGGTGTT GGTCGTCTCG GCCCGGACAT TCGATCTTCA 420

GGGCCT 426

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1521 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGCAGCCTT CAATGTCTTT TCTTATCGGC TTCGGAACAT TGGTGTTGGT CCTCTCGGCC 60

CGGACATTCG ATCTTCAGGG CCTTAGCTGC AATACTGACT CCACTCCTGG ACTGATTGAC 120

CTGGAGATAA GGCGACTTTG CCACACCCCA ACGGAAAATG TCATTTCATG CGAGGTTAGT 180

TATCTCAACC ACACGACTAT TAGCCTCCCG GCAGTCCACA CATCATGCCT CAAGTACCAC 240

TGCAAAACCT ATTGGGGATT CTTTGGTAGC TACAGCGCTG ACCGAATCAT AAATCGGTAC 300

ACTGGTACTG TTAAGGGTTG TCTAAACAAC TCAGCACCAG AGGACCCCTT CGAGTGCAAC 360

TGGTTCTACT GCTGCTCGGC GATTACAACA GAGATCTGCC GATGCTCTAT TACAAATGTC 420

ACGGTGGCTG TGCAAACATT CCCACCGTTC ATGTACTGCA GTTTTGCAGA CTGCAGTACC 480

GTGAGCCAAC AGGAGCTAGA GAGTGGAAAG GCAATGCTGA GCGATGGCAG TACATTAACT 540

TATACCCCGT ATATCCTACA GTCAGAAGTC GTGAACAAAA CCCTCAATGG GACCATACTC 600

TGCAACTCAT CCTCTAAGAT AGTTTCCTTC GATGAATTTA GGCGTTCATA CTCCCTAACG 660

AATGGTAGTT ACCAGAGCTC ATCAATCAAT GTGACGTGTG CAAACTACAC GTCGTCCTGC 720

CGGCCCAGGT TGAAAAGGCG GCGTAGGGAC ACCCAGCAGA TTGAGTATCT AGTTCACAAG 780

CTTAGGCCCA CACTGAAAGA TGCATGGGAG GACTGTGAGA TCCTCCAGTC TCTGCTCCTA 840

GGGGTGTTTG GTACTGGGAT CGCAAGTGCT TCTCAATTTT TGAGGAGCTG GCTCAACCAC 900

CCTGACATCA TCGGGTATAT AGTTAATGGA GTTGGGGTTG TCTGGCAATG CCATCGTGTT 960

AATGTCACGT TCATGGCGTG GAATGAGTCC ACCTATTACC CTCCAGTAGA TTACAATGGG 1020

CGGAAGTACT TCCTGAATGA TGAGGGAAGG TTACAAACAA ACACCCCCGA GGCAAGGCCA 1080

GGGCTTAAGC GGGTCATGTG GTTCGGCAGG TACTTCCTAG GGACAGTAGG GTCTGGGGTG 1140

AAACCGAGGA GGATTCGGTA CAATAAGACC TCACATGACT ACCACCTGGA GGAGTTTGAG 1200

GCAAGTCTCA ACATGACCCC TCAGACCAGT ATCGCCTCGG GTCATGAGAC AGACCGCATA 1260

AATCATGCCT ACGGAACGCA GGCTGATCTC CTTCCATACA CCAGGTCTAG TAATATAACA 1320

TCTACGGATA CAGGCTCAGG CTGGGTGCAC ATCGGCCTAC CCTCATTTGC TTTCCTCAAT 1380

CCCCTCGGGT GGCTCAGGGA CCTACTTGCA TGGGCAGCCT GGTTGGGTGG GGTTCTATAC 1440

TTAATAAGTC TTTGTGTTTC CTTACCAGCC TCCTTCGCGA GGAGGAGACG CCTCGGCCGG 1500

TGGCAGGAAT AAACCGTACC G 1521

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1521 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGCAGCCTT CAATGTCTTT TCTTATCGGC TTCGGAACAT TGGTGTTGGT CCTCTCGGCC 60

CGGACATTCG ATCTTCAGGG CCTTAGCTGC AATACTGACT CCACTCCTGG ACTGATTGAC 120

CTGGAGATAA GGCGACTTTG CCACACCCCA ACGGAAAATG TCATTTCATG CGAGGTTAGT 180

TATCTCAACC ACACGACTAT TAGCCTCCCG GCAGTCCACA CATCATGCCT CAAGTACCAC 240

TGCAAAACCT ATTGGGGATT CTTTGGTAGC TACAGCGCTG ACCGAATCAT AAATCGGTAC 300

ACTGGTACTG TTAAGGGTTG TCTAAACAAC TCAGCACCAG AGGACCCCTT CGAGTGCAAC 360

TGGTTCTACT GCTGCTCGGC GATTACAACA GAGATCTGCC GATGCTCTAT TACAAATGTC 420

ACGGTGGCTG TGCAAACATT CCCACCGTTC ATGTACTGCA GTTTTGCAGA CTGCAGTACC 480

GTGAGCCAAC AGGAGCTAGA GAGTGGAAAG GCAATGCTGA GCGATGGCAG TACATTAACT 540

TATACCCCGT ATATCCTACA GTCAGAAGTC GTGAACAAAA CCCTCAATGG GACCATACTC 600

TGCAACTCAT CCTCTAAGAT AGTTTCCTTC GATGAATTTA GGCGTTCATA CTCCCTAACG 660

AATGGTAGTT ACCAGAGCTC ATCAATCAAT GTGACGTGTG CAAACTACAC GTCGTCCTGC 720

CGGCCCAGGT TGAAAAGGCG GCGTAGGGAC ACCCAGCAGA TTGAGTATCT AGTTCACAAG 780

CTTAGGCCCA CACTGAAAGA TGCATGGGAG GACTGTGAGA TCCTCCAGTC TCTGCTCCTA 840

GGGGTGTTTG GTACTGGGAT CGCAAGTGCT TCTCAATTTT TGAGGAGCTG GCTCAACCAC 900

CCTGACATCA TCGGGTATAT AGTTAATGGA GTTGGGGTTG TCTGGCAATG CCATCGTGTT 960

AATGTCACGT TCATGACGTG GAATGAGTCC ACCTATTACC CTCCAGTAGA TTACAATGGG 1020

CGGAAGTACT TCCTGAATGA TGAGGGAAGG TTACAAACAA ACACCCCCGA GGCAAGGCCA 1080

GGGCTTAAGC GGGTCATGTG GTTCGGCAGG TACTTCCTAG GGACAGTAGG GTCTGGGGTG 1140

AAACCGAGGA GGATTCGGTA CAATAAGACC TCACATGACT ACCACCTGGA GGAGTTTGAG 1200

GCAAGTCTCA ACATGACCCC TCAGACCAGT ATCACCTCGG GTCATGAGAC AGACCCCATA 1260

AATCATGCCT ACGGAACGCA GGCTGATCTC CTTCCATACA CCAGGTCTAG TAATATAACA 1320

TCTACGGATA CAGGCTCAGG CTGGGTGCAC ATCGGCCTAC CCTCATTTGC TTTCCTCAAT 1380

CCCCTCGGGT GGCTCAGGGA CCTACTTGCA TGGGCAGCCT GGTTGGGTGG GGTTCTATAC 1440

TTAATAAGTC TTTGTGTTTC CTTACCAGCC TCCTTCGCGA GGAGGAGACG CCTCGGCCGG 1500

TTGCAGGAAT AAACCGTACC G 1521

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1521 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGCAGCCTT CAATGTCTTT TCTTATCGGC TTCGGAACAT TGGTGTTGGT CCTCTCGGCC 60

CGGACATTCG ATCTTCAGGG CCTTAGCTGC AATACTGACT CCACTCCTGG ACTGATTGAC 120

CTGGAGATAA GGCGACTTTG CCACACCCCA ACGGAAAATG TCATTTCATG CGAGGTTAGT 180

TATCTCAACC ACACGACTAT TAGCCTCCCG GCAGTCCACA CATCATGCCT CAAGTACCAC 240

TGCAAAACCT ATTGGGGATT CTTTGGTAGC TACAGCGCTG ACCGAATCAT AAATCGGTAC 300

ACTGGTACTG TTAAGGGTTG TCTAAACAAC TCAGCACCAG AGGACCCCTT CGAGTGCAAC 360

TGGTTCTACT GCTGCTCGGC GATTACAACA GAGATCTGCC GATGCTCTAT TACAAATGTC 420

ACGGTGGCTG TGCAAACATT CCCACCGTTC ATGTACTGCA GTTTTGCAGA CTGCAGTACC 480

GTGAGCCAAC AGGAGCTAGA GAGTGGAAAG GCAATGCTGA GCGATGGCAG TACATTAACT 540

TATACCCCGT ATATCCTACA GTCAGAAGTC GTGAACAAAA CCCTCAATGG GACCATACTC 600

TGCAACTCAT CCTCTAAGAT AGTTTCCTTC GATGAATTTA GGCGTTCATA CTCCCTAACG 660

AATGGTAGTT ACCAGAGCTC ATCAATCAAT GTGACGTGTG CAAACTACAC GTCGTCCTGC 720

CGGCCCAGGT TGAAAAGGCG GCGTAGGGAC ACCCAGCAGA TTGAGTATCT AGTTCACAAG 780

CTTAGGCCCA CACTGAAAGA TGCATGGGAG GACTGTGAGA TCCTCCAGTC TCTGCTCCTA 840

GGGGTGTTTG GTACTGGGAT CGCAAGTGCT TCTCAATTTT TGAGGAGCTG GCTCAACCAC 900

CCTGACATCA TCGGGTATAT AGTTAATGGA GTTGGGGTTG TCTGGCAATG CCATCGTGTT 960

AATGTCACGT TCATGACGTG GAATGAGTCC ACCTATTACC CTCCAGTAGA TTACAATGGG 1020

CGGAAGTACT TCCTGAATGA TGAGGGAAGG TTACAAACAA ACACCCCCGA GGCAAGGCCA 1080

GGGCTTAAGC GGGTCATGTG GTTCGGCAGG TACTTCCTAG GGACAGTAGG GTCTGGGGTG 1140

AAACCGAGGA GGATTCGGTA CAATAAGACC TCACATGACT ACCACCTGGA GGAGTTTGAG 1200

GCAAGTCTCA ACATGACCCC TCAGACCAGT ATCGCCTCGG GTCATGAGAC AGACCCCATA 1260

AATCATGCCT ACGGAACGCA GGCTGATCTC CTTCCATACA CCAGGTCTAG TAATATAACA 1320

TCTACGGATA CAGGCTCAGG CTGGGTGCAC ATCGGCCTAC CCTCATTTGC TTTCCTCAAT 1380

CCCCTCGGGT GGCTCAGGGA CCTACTTGCA TGGGCAGCCT GGTTGGGTGG GGTTCTATAC 1440

TTAATAAGTC TTTGTGTTTC CTTACCAGCC TCCTTCGCGA GGAGGAGACG CCTCGGCCGG 1500

TGGCAGGAAT AAACCGTACC G 1521

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTCAYACAGT AACGCCYAGC CTTGTGTTTC TATGTTTGCT AATCCCAGGA CTGCACGCTG 60

CGTTTGTTCA CGGAGGGGTG CCTCGTGAAT CYTACCTGTC GACGCCTRTY ACGCGTGGRG 120

AACAGACTGT YGTTAAGACT GCRRAGTTTT ACGGGGAAAA GACRACRCAG CGTGATCTCA 180

CCGAGCTGGA GATCTCCTCT ATMTTCAGCC ATTGTTGCTC ATTACTAATW GGGGTTGTGA 240

TAGGATCGTC RTCTAAGATY AAAGCAGRAG CCGAGCAGAT CAAGAAAAGG TTTAAAACTA 300

TGATGGCAGC CKTAAACCGG CCATCCCATG GTGAGACTGC TACACTACTY CAGATGTTTA 360

ATCCACATGA GGCTATAGAT TGGATTAACG GCCARCCCTG GGTAGGCTCC TTTGTGTTGY 420

CTCTACTAAC TACAGACTTT GAGTCCCCAG GTAAAGAATT YATGGAYCAG ATTAARCTTG 480

TCGCAAGTTA TGCRCAGATG ACTACGTACA CTACTATAAA GGAGTACCTC GCAGAATGYA 540

TGGATGCTAC CCTTACAATC CCYGTAGTTG C 571

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTCATACAGT AACGCCCAGC CTTGTGTTTC TATGTTTGCT AATCCCAGGA CTGCACGCTG 60

CGTTTGTTCA CGGAGGGGTG CCTCGTGAAT CCTACCTGTC GACGCCTGTC ACGCGTGGAG 120

AACAGACTGT TGTTAAGACT GCGAAGTTTT ACGGGGAAAA GACGACGCAG CGTGATCTCA 180

CCGAGCTGGA GATCTCCTCT ATCTTCAGCC ATTGTTGCTC ATTACTAATA GGGGTTGTGA 240

TAGGATCGTC GTCTAAGATC AAAGCAGGAG CCGAGCAGAT CAAGAAAAGG TTTAAAACTA 300

TGATGGCAGC CTTAAACCGG CCATCCCATG GTGAGACTGC TACACTACTC CAGATGTTTA 360

ATCCACATGA GGCTATAGAT TGGATTAACG GCCAACCCTG GGTAGGCTCC TTTGTGTTGC 420

CTCTACTAAC TACAGACTTT GAGTCCCCAG GTAAAGAATT TATGGACCAG ATTAAGCTTG 480

TCGCAAGTTA TGCACAGATG ACTACGTACA CTACTATAAA GGAGTACCTC GCAGAATGCA 540

TGGATGCTAC CCTTACAATC CCTGTAGTTG C 571

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) *HYPOTHETICAL: NO*

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTCATACAGT AACGCCCAGC CTTGTGTTTC TATGTTTGCT AATCCCAGGA CTGCACGCTG 60

CGTTTGTTCA CGGAGGGGTG CCTCGTGAAT CCTACCTGTC GACGCCTATC ACGCGTGGAG 120

AACAGACTGT TGTTAAGACT GCGGAGTTTT ACGGGGAAAA GACGACGCAG CGTGATCTCA 180

CCGAGCTGGA GATCTCCTCT ATCTTCAGCC ATTGTTGCTC ATTACTAATA GGGGTTGTGA 240

TAGGATCGTC GTCTAAGATC AAAGCAGAAG CCGAGCAGAT CAAGAAAAGG TTTAAAACTA 300

TGATGGCAGC CGTAAACCGG CCATCCCATG GTGAGACTGC TACACTACTC CAGATGTTTA 360

ATCCACATGA GGCTATAGAT TGGATTAACG GCCAACCCTG GGTAGGCTCC TTTGTGTTGT 420

CTCTACTAAC TACAGACTTT GAGTCCCCAG GTAAAGAATT TATGGACCAG ATTAAGCTTG 480

TCGCAAGTTA TGCACAGATG ACTACGTACA CTACTATAAA GGAGTACCTC GCAGAATGCA 540

TGGATGCTAC CCTTACAATC CCTGTAGTTG C 571

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTCATACAGT AACGCCCAGC CTTGTGTTTC TATGTTTGCT AATCCCAGGA CTGCACGCTG 60

CGTTTGTTCA CGGAGGGGTG CCTCGTGAAT CCTACCTGTC GACGCCTATC ACGCGTGGAG 120

AACAGACTGT TGTTAAGACT GCGAAGTTTT ACGGGGAAAA GACGACGCAG CGTGATCTCA 180

CCGAGCTGGA GATCTCCTCT ATCTTCAGCC ATTGTTGCTC ATTACTAATA GGGGTTGTGA 240

TAGGATCGTC GTCTAAGATC AAAGCAGGAG CCGAGCAGAT CAAGAAAAGG TTTAAAACTA 300

TGATGGCAGC CTTAAACCGG CCATCCCATG GTGAGACTGC TACACTACTC CAGATGTTTA 360

ATCCACATGA GGCTATAGAT TGGATTAACG GCCAACCCTG GGTAGGCTCC TTTGTGTTGT 420

CTCTACTAAC TACAGACTTT GAGTCCCCAG GTAAAGAATT TATGGACCAG ATTAAGCTTG 480

TCGCAAGTTA TGCACAGATG ACTACGTACA CTACTATAAA GGAGTACCTC GCAGAATGCA 540

TGGATGCTAC CCTTACAATC CCTGTAGTTG C 571

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 689 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TGACCATGAG CTCAACGGCY CTAACYCAYC TTCTTAACCG GCTATCACAT ACTATCACTA 60

AGGGTGACTC CTTTGTTATT AACYTWGAYT ATAGYTCCTG GTGCAACGGT TTCCGACCAG 120

AACTRCARGC CCCAMTCTGT CGTCAGTTGG ATCAGATGTT CAATTGCGGG TACTTCTTCA 180

GGACTGGGTG CACACTGCCA TGCTTTACCA CGTTTATTAT TCARGACAGR TTCAACCCGC 240

CCTATTCCYT CMGTGGTGAG CCCGTTGAAG ACGGWGTYAC ATGCGCGGTT GGGACTAARA 300

CAATGGGRGA GGGYATGAGG CAGAAACTAT GGACAATYCT TACGAGCTGC TGGGAGATAA 360

TTGCTCTTCG GGAAATTAAC GTGACGTTTA AYATACTAGG CCARGGTGAT AATCAGACAA 420

TCATYRTACA TAAATCTGCA AGCCAAAATA AYCAGCTATT AGCGGAGCGA GCAYTRGGRG 480

CYYTGTACAA GCATGCTAGA TTAGCTGGCC ATAACCTYAA GGTAGARGAA TGYTGGGTGT 540

CAGATTGTCT GTATGAGTAT GGAAAGAAGC TYTTCTTCCG TGGTGTACCT GTCCCRGGCT 600

GTTTGAAGCA GCTCTCRCGG GTGACGGAYT CYACTGGRGA GYTATTCCCA AACCTATACT 660

CAAAGTTAGC CTGCTWAACA TCATCRTGY 689

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 689 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGACCATGAG CTCAACGGCT CTAACTCACC TTCTTAACCG GCTATCACAT ACTATCACTA 60

AGGGTGACTC CTTTGTTATT AACCTTGACT ATAGTTCCTG GTGCAACGGT TTCCGACCAG 120

AACTGCAGGC CCCAATCTGT CGTCAGTTGG ATCAGATGTT CAATTGCGGG TACTTCTTCA 180

GGACTGGGTG CACACTGCCA TGCTTTACCA CGTTTATTAT TCAAGACAGG TTCAACCCGC 240

CCTATTCCCT CAGTGGTGAG CCCGTTGAAG ACGGAGTTAC ATGCGCGGTT GGGACTAAAA 300

CAATGGGGGA GGGCATGAGG CAGAAACTAT GGACAATCCT TACGAGCTGC TGGGAGATAA 360

TTGCTCTTCG GGAAATTAAC GTGACGTTTA ACATACTAGG CCAAGGTGAT AATCAGACAA 420

TCATCATACA TAAATCTGCA AGCCAAAATA ACCAGCTATT AGCGGAGCGA GCACTAGGGG 480

CCCTGTACAA GCATGCTAGA TTAGCTGGCC ATAACCTCAA GGTAGAGGAA TGCTGGGTGT 540

CAGATTGTCT GTATGAGTAT GGAAAGAAGC TTTTCTTCCG TGGTGTACCT GTCCCGGGCT 600

GTTTGAAGCA GCTCTCACGG GTGACGGATT CTACTGGAGA GCTATTCCCA AACCTATACT 660

CAAAGTTAGC CTGCTTAACA TCATCATGC 689

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 689 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGACCATGAG CTCAACGGCT CTAACTCACC TTCTTAACCG GCTATCACAT ACTATCACTA 60

AGGGTGACTC CTTTGTTATT AACCTTGACT ATAGTTCCTG GTGCAACGGT TTCCGACCAG 120

AACTGCAGGC CCCAATCTGT CGTCAGTTGG ATCAGATGTT CAATTGCGGG TACTTCTTCA 180

GGACTGGGTG CACACTGCCA TGCTTTACCA CGTTTATTAT TCAAGACAGG TTCAACCCGC 240

CCTATTCCCT CAGTGGTGAG CCCGTTGAAG ACGGAGTTAC ATGCGCGGTT GGGACTAAAA 300

CAATGGGGGA GGGCATGAGG CAGAAACTAT GGACAATCCT TACGAGCTGC TGGGAGATAA 360

TTGCTCTTCG GGAAATTAAC GTGACGTTTA ACATACTAGG CCAAGGTGAT AATCAGACAA 420

TCATCATACA TAAATCTGCA AGCCAAAATA ACCAGCTATT AGCGGAGCGA GCACTAGGGG 480

CCCTGTACAA GCATGCTAGA TTAGCTGGCC ATAACCTCAA GGTAGAGGAA TGCTGGGTGT 540

CAGATTGTCT GTATGAGTAT GGAAAGAAGC TTTTCTTCCG TGGTGTACCT GTCCCGGGCT 600

GTTTGAAGCA GCTCTCACGG GTGACGGATT CTACTGGAGA GCTATTCCCA AACCTATACT 660

CAAAGTTAGC CTGCTAAACA TCATCATGC 689

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Ala Thr Glu Pro Ser Ser Leu Val Asp Ser Leu Glu Asp Glu Glu
1 5 10 15

Asp Pro Gln Thr Leu Arg Arg Glu Arg Ser Gly Ser Pro Arg Pro Arg
20 25 30

Lys Val Pro Arg Asn Ala Leu Thr Gln Pro Val Asp Gln Leu Leu Lys
35 40 45

Asp Leu Arg Lys Asn Pro Ser Met Ile Ser Asp Pro Asp Gln Arg Thr
50 55 60

Gly Arg Glu Gln Leu Ser Asn Asp Glu Leu Ile Lys Lys Leu Val Thr
65 70 75 80

Glu Leu Ala Glu Asn Ser Met Ile Glu Ala Glu Glu Val Arg Gly Thr
85 90 95

Leu Gly Asp Ile Ser Ala Arg Ile Glu Ala Gly Phe Glu Ser Leu Ser
100 105 110

Ala Leu Gln Val Glu Thr Ile Gln Thr Ala Gln Arg Cys Asp Tyr Ser
115 120 125

Asp Ser Ile Arg Ile Leu Gly Glu Asn Ile Lys Ile Leu Asp Arg Ser
130 135 140

Met Lys Thr Met Met Glu Thr Met Lys Leu Met Met Glu Lys Val Asp
145 150 155 160

Leu Leu Tyr Ala Ser Thr Ala Val Gly Thr Ser Ala Pro Met Leu Pro
165 170 175

Ser His Pro Ala Pro Pro Arg Ile Tyr Pro Gln Leu Pro Ser Ala Pro
180 185 190

Thr Thr Asp Glu Trp Asp Ile Ile Pro
195 200

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ala Thr Gly Pro Ser Ser Leu Val Asp Ser Leu Glu Asp Glu Glu
1 5 10 15

Asp Pro Gln Thr Leu Arg Arg Glu Arg Ser Gly Ser Pro Arg Pro Arg
20 25 30

Lys Val Pro Arg Asn Ala Leu Thr Gln Pro Val Asp Gln Leu Leu Lys
35 40 45

Asp Leu Arg Lys Asn Pro Ser Met Ile Ser Asp Pro Asp Gln Arg Thr
50 55 60

Gly Arg Glu Gln Leu Ser Asn Asp Glu Leu Ile Lys Lys Leu Val Thr
65 70 75 80

Glu Leu Ala Glu Asn Ser Met Ile Glu Ala Glu Glu Val Arg Gly Thr
85 90 95

Leu Gly Asp Ile Ser Ala Arg Ile Glu Ala Gly Phe Glu Ser Leu Ser
100 105 110

Ala Leu Gln Val Glu Thr Ile Gln Thr Ala Gln Arg Cys Asp His Ser
115 120 125

Asp Ser Ile Arg Ile Leu Gly Glu Asn Ile Lys Ile Leu Asp Arg Ser
130 135 140

Met Lys Thr Met Met Glu Thr Met Lys Leu Met Met Glu Lys Val Asp
145 150 155 160

Leu Leu Tyr Ala Ser Thr Ala Val Gly Thr Ser Ala Pro Met Leu Pro
165 170 175

Ser His Pro Ala Pro Pro Arg Ile Tyr Pro Gln Leu Pro Ser Ala Pro
180 185 190

Thr Thr Asp Glu Trp Asp Ile Ile Pro
195 200

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ala Thr Glu Pro Ser Ser Leu Val Asp Ser Leu Glu Asp Glu Glu
1 5 10 15

Asp Pro Gln Thr Leu Arg Arg Glu Arg Ser Gly Ser Pro Arg Pro Arg
20 25 30

Lys Val Pro Arg Asn Ala Leu Thr Gln Pro Val Asp Gln Leu Leu Lys
35 40 45

Asp Leu Arg Lys Asn Pro Ser Met Ile Ser Asp Pro Asp Gln Arg Thr
50 55 60

Gly Arg Glu Gln Leu Ser Asn Asp Glu Leu Ile Lys Lys Leu Val Thr
65 70 75 80

Glu Leu Ala Glu Asn Ser Met Ile Glu Ala Glu Glu Val Arg Gly Thr
85 90 95

Leu Gly Asp Ile Ser Ala Arg Ile Glu Ala Gly Phe Glu Ser Leu Ser
100 105 110

Ala Leu Gln Val Glu Thr Ile Gln Thr Ala Gln Arg Cys Asp His Ser
115 120 125

Asp Ser Ile Arg Ile Leu Gly Glu Asn Ile Lys Ile Leu Asp Arg Ser
130 135 140

Met Lys Thr Met Met Glu Thr Met Lys Leu Met Met Glu Lys Val Asp
145 150 155 160

Leu Leu Tyr Ala Ser Thr Ala Val Gly Thr Ser Ala Pro Met Leu Pro
165 170 175

Ser His Pro Ala Pro Pro Arg Ile Tyr Pro Gln Leu Pro Ser Ala Pro
180 185 190

Thr Thr Asp Glu Trp Asp Ile Ile Pro
195 200

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Asn Ser Lys His Ser Tyr Val Glu Leu Lys Asp Lys Val Ile Val
1 5 10 15

Pro Gly Trp Pro Thr Leu Met Leu Glu Ile Asp Phe Val Gly Gly Thr
20 25 30

Ser Arg Asn Gln Phe Leu Asn Ile Pro Phe Leu Ser Val Lys Glu Pro
35 40 45

Leu Gln Leu Pro Arg Glu Lys Lys Leu Thr Asp Tyr Phe Thr Ile Asp
50 55 60

Val Glu Pro Ala Gly His Ser Leu Val Asn Ile Tyr Phe Gln Ile Asp
65 70 75 80

Asp Phe Leu Leu Leu Thr Leu Asn Ser Leu Ser Val Tyr Lys Asp Pro
85 90 95

Ile Arg Lys Tyr Met Phe Leu Arg Leu Asn Lys Asp Gln Ser Lys His
100 105 110

Ala Ile Asn Ala Ala Phe Asn Val Phe Ser Tyr Arg Leu Arg Asn Ile
115 120 125

Gly Val Gly Pro Leu Gly Pro Asp Ile Arg Ser Ser Gly Pro
130 135 140

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Asn Ser Lys His Ser Tyr Val Glu Leu Lys Asp Lys Val Ile Val
1 5 10 15

Pro Gly Trp Pro Thr Leu Met Leu Glu Ile Asp Phe Val Gly Gly Thr
20 25 30

Ser Arg Asn Gln Phe Leu Asn Ile Pro Phe Leu Ser Val Lys Glu Pro
35 40 45

Leu Gln Leu Pro Arg Glu Lys Lys Leu Thr Asp Tyr Phe Thr Ile Asp
50 55 60

Val Glu Pro Ala Gly His Ser Leu Val Asn Ile Tyr Phe Gln Ile Asp
65 70 75 80

Asp Phe Leu Leu Leu Thr Leu Asn Ser Leu Ser Val Tyr Lys Asp Pro
85 90 95

Ile Arg Lys Tyr Met Phe Leu Arg Leu Asn Lys Asp Gln Ser Lys His
100 105 110

Ala Ile Asn Ala Ala Phe Asn Val Phe Ser Tyr Arg Leu Arg Asn Ile
115 120 125

Gly Val Gly Pro Leu Gly Pro Asp Ile Arg Ser Ser Gly Pro
130 135 140

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Asn Ser Lys His Ser Tyr Val Glu Leu Lys Asp Lys Val Ile Val
1 5 10 15

Pro Gly Trp Pro Thr Leu Met Leu Glu Ile Gly Phe Val Gly Gly Thr
20 25 30

Ser Arg Asn Gln Phe Leu Asn Ile Pro Phe Leu Ser Val Lys Glu Pro

35 40 45

Leu Gln Leu Pro Arg Glu Lys Lys Leu Thr Asp Tyr Phe Thr Ile Asp
50 55 60

Val Glu Pro Ala Gly His Ser Leu Val Asn Ile Tyr Phe Gln Ile Asp
65 70 75 80

Asp Phe Leu Leu Leu Thr Leu Asn Ser Leu Ser Val Tyr Lys Asp Pro
85 90 95

Ile Arg Lys Tyr Met Phe Leu Arg Leu Asn Lys Asp Gln Ser Lys His
100 105 110

Ala Ile Asn Ala Ala Phe Asn Val Phe Ser Tyr Arg Leu Arg Asn Ile
115 120 125

Gly Val Gly Pro Leu Gly Pro Asp Ile Arg Ser Ser Gly Pro
130 135 140

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 503 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Gln Pro Ser Met Ser Phe Leu Ile Gly Phe Gly Thr Leu Val Leu
1 5 10 15

Val Leu Ser Ala Arg Thr Phe Asp Leu Gln Gly Leu Ser Cys Asn Thr
20 25 30

Asp Ser Thr Pro Gly Leu Ile Asp Leu Glu Ile Arg Arg Leu Cys His
35 40 45

Thr Pro Thr Glu Asn Val Ile Ser Cys Glu Val Ser Tyr Leu Asn His
50 55 60

Thr Thr Ile Ser Leu Pro Ala Val His Thr Ser Cys Leu Lys Tyr His
65 70 75 80

Cys Lys Thr Tyr Trp Gly Phe Phe Gly Ser Tyr Ser Ala Asp Arg Ile
85 90 95

Ile Asn Arg Tyr Thr Gly Thr Val Lys Gly Cys Leu Asn Asn Ser Ala
100 105 110

Pro Glu Asp Pro Phe Glu Cys Asn Trp Phe Tyr Cys Cys Ser Ala Ile
115 120 125

Thr Thr Glu Ile Cys Arg Cys Ser Ile Thr Asn Val Thr Val Ala Val
130 135 140

Gln Thr Phe Pro Pro Phe Met Tyr Cys Ser Phe Ala Asp Cys Ser Thr
145 150 155 160

Val Ser Gln Gln Glu Leu Glu Ser Gly Lys Ala Met Leu Ser Asp Gly
165 170 175

Ser Thr Leu Thr Tyr Thr Pro Tyr Ile Leu Gln Ser Glu Val Val Asn
180 185 190

Lys Thr Leu Asn Gly Thr Ile Leu Cys Asn Ser Ser Ser Lys Ile Val
195 200 205

Ser Phe Asp Glu Phe Arg Arg Ser Tyr Ser Leu Thr Asn Gly Ser Tyr
210 215 220

Gln Ser Ser Ser Ile Asn Val Thr Cys Ala Asn Tyr Thr Ser Ser Cys
225 230 235 240

Arg Pro Arg Leu Lys Arg Arg Arg Arg Asp Thr Gln Gln Ile Glu Tyr
245 250 255

Leu Val His Lys Leu Arg Pro Thr Leu Lys Asp Ala Trp Glu Asp Cys
260 265 270

Glu Ile Leu Gln Ser Leu Leu Leu Gly Val Phe Gly Thr Gly Ile Ala
275 280 285

Ser Ala Ser Gln Phe Leu Arg Ser Trp Leu Asn His Pro Asp Ile Ile
290 295 300

Gly Tyr Ile Val Asn Gly Val Gly Val Val Trp Gln Cys His Arg Val
305 310 315 320

Asn Val Thr Phe Met Thr Trp Asn Glu Ser Thr Tyr Tyr Pro Pro Val
325 330 335

Asp Tyr Asn Gly Arg Lys Tyr Phe Leu Asn Asp Glu Gly Arg Leu Gln
340 345 350

Thr Asn Thr Pro Glu Ala Arg Pro Gly Leu Lys Arg Val Met Trp Phe
355 360 365

Gly Arg Tyr Phe Leu Gly Thr Val Gly Ser Gly Val Lys Pro Arg Arg
370 375 380

Ile Arg Tyr Asn Lys Thr Ser His Asp Tyr His Leu Glu Glu Phe Glu
385 390 395 400

Ala Ser Leu Asn Met Thr Pro Gln Thr Ser Ile Thr Ser Gly His Glu
405 410 415

Thr Asp Pro Ile Asn His Ala Tyr Gly Thr Gln Ala Asp Leu Leu Pro
420 425 430

Tyr Thr Arg Ser Ser Asn Ile Thr Ser Thr Asp Thr Gly Ser Gly Trp
435 440 445

Val His Ile Gly Leu Pro Ser Phe Ala Phe Leu Asn Pro Leu Gly Trp
450 455 460

Leu Arg Asp Leu Leu Ala Trp Ala Ala Trp Leu Gly Gly Val Leu Tyr
465 470 475 480

Leu Ile Ser Leu Cys Val Ser Leu Pro Ala Ser Phe Ala Arg Arg Arg
485 490 495

Arg Leu Gly Arg Leu Gln Glu
500

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 503 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Gln Pro Ser Met Ser Phe Leu Ile Gly Phe Gly Thr Leu Val Leu
1 5 10 15

Val Leu Ser Ala Arg Thr Phe Asp Leu Gln Gly Leu Ser Cys Asn Thr
20 25 30

Asp Ser Thr Pro Gly Leu Ile Asp Leu Glu Ile Arg Arg Leu Cys His
35 40 45

Thr Pro Thr Glu Asn Val Ile Ser Cys Glu Val Ser Tyr Leu Asn His
50 55 60

Thr Thr Ile Ser Leu Pro Ala Val His Thr Ser Cys Leu Lys Tyr His
65 70 75 80

Cys Lys Thr Tyr Trp Gly Phe Phe Gly Ser Tyr Ser Ala Asp Arg Ile
85 90 95

Ile Asn Arg Tyr Thr Gly Thr Val Lys Gly Cys Leu Asn Asn Ser Ala
100 105 110

Pro Glu Asp Pro Phe Glu Cys Asn Trp Phe Tyr Cys Cys Ser Ala Ile
115 120 125

Thr Thr Glu Ile Cys Arg Cys Ser Ile Thr Asn Val Thr Val Ala Val
130 135 140

Gln Thr Phe Pro Pro Phe Met Tyr Cys Ser Phe Ala Asp Cys Ser Thr
145 150 155 160

Val Ser Gln Gln Glu Leu Glu Ser Gly Lys Ala Met Leu Ser Asp Gly
165 170 175

Ser Thr Leu Thr Tyr Thr Pro Tyr Ile Leu Gln Ser Glu Val Val Asn
180 185 190

Lys Thr Leu Asn Gly Thr Ile Leu Cys Asn Ser Ser Ser Lys Ile Val
195 200 205

Ser Phe Asp Glu Phe Arg Arg Ser Tyr Ser Leu Thr Asn Gly Ser Tyr
210 215 220

Gln Ser Ser Ser Ile Asn Val Thr Cys Ala Asn Tyr Thr Ser Ser Cys
225 230 235 240

Arg Pro Arg Leu Lys Arg Arg Arg Arg Asp Thr Gln Gln Ile Glu Tyr
245 250 255

Leu Val His Lys Leu Arg Pro Thr Leu Lys Asp Ala Trp Glu Asp Cys
260 265 270

Glu Ile Leu Gln Ser Leu Leu Leu Gly Val Phe Gly Thr Gly Ile Ala
275 280 285

Ser Ala Ser Gln Phe Leu Arg Ser Trp Leu Asn His Pro Asp Ile Ile
290 295 300

Gly Tyr Ile Val Asn Gly Val Gly Val Val Trp Gln Cys His Arg Val
305 310 315 320

Asn Val Thr Phe Met Thr Trp Asn Glu Ser Thr Tyr Tyr Pro Pro Val
325 330 335

Asp Tyr Asn Gly Arg Lys Tyr Phe Leu Asn Asp Glu Gly Arg Leu Gln
340 345 350

Thr Asn Thr Pro Glu Ala Arg Pro Gly Leu Lys Arg Val Met Trp Phe
355 360 365

Gly Arg Tyr Phe Leu Gly Thr Val Gly Ser Gly Val Lys Pro Arg Arg
370 375 380

Ile Arg Tyr Asn Lys Thr Ser His Asp Tyr His Leu Glu Glu Phe Glu
385 390 395 400

Ala Ser Leu Asn Met Thr Pro Gln Thr Ser Ile Ala Ser Gly His Glu
405 410 415

Thr Asp Pro Ile Asn His Ala Tyr Gly Thr Gln Ala Asp Leu Leu Pro
420 425 430

Tyr Thr Arg Ser Ser Asn Ile Thr Ser Thr Asp Thr Gly Ser Gly Trp
435 440 445

Val His Ile Gly Leu Pro Ser Phe Ala Phe Leu Asn Pro Leu Gly Trp
450 455 460

Leu Arg Asp Leu Leu Ala Trp Ala Ala Trp Leu Gly Gly Val Leu Tyr
465 470 475 480

Leu Ile Ser Leu Cys Val Ser Leu Pro Ala Ser Phe Ala Arg Arg Arg
485 490 495

Arg Leu Gly Arg Trp Gln Glu
500

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

His Thr Val Thr Pro Ser Leu Val Phe Leu Cys Leu Leu Ile Pro Gly
1 5 10 15

Leu His Ala Ala Phe Val His Gly Gly Val Pro Arg Glu Ser Tyr Leu
20 25 30

Ser Thr Pro Val Thr Arg Gly Glu Gln Thr Val Val Lys Thr Ala Lys
35 40 45

Phe Tyr Gly Glu Lys Thr Thr Gln Arg Asp Leu Thr Glu Leu Glu Ile
50 55 60

Ser Ser Ile Phe Ser His Cys Cys Ser Leu Leu Ile Gly Val Val Ile
65 70 75 80

Gly Ser Ser Ser Lys Ile Lys Ala Gly Ala Glu Gln Ile Lys Lys Arg
85 90 95

Phe Lys Thr Met Met Ala Ala Leu Asn Arg Pro Ser His Gly Glu Thr
100 105 110

Ala Thr Leu Leu Gln Met Phe Asn Pro His Glu Ala Ile Asp Trp Ile
115 120 125

Asn Gly Gln Pro Trp Val Gly Ser Phe Val Leu Pro Leu Leu Thr Thr
130 135 140

Asp Phe Glu Ser Pro Gly Lys Glu Phe Met Asp Gln Ile Lys Leu Val
145 150 155 160

Ala Ser Tyr Ala Gln Met Thr Thr Tyr Thr Thr Ile Lys Glu Tyr Leu
165 170 175

Ala Glu Cys Met Asp Ala Thr Leu Thr Ile Pro Val Val
180 185

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

His Thr Val Thr Pro Ser Leu Val Phe Leu Cys Leu Leu Ile Pro Gly
1 5 10 15

Leu His Ala Ala Phe Val His Gly Gly Val Pro Arg Glu Ser Tyr Leu
20 25 30

Ser Thr Pro Ile Thr Arg Gly Glu Gln Thr Val Val Lys Thr Ala Glu
35 40 45

Phe Tyr Gly Glu Lys Thr Thr Gln Arg Asp Leu Thr Glu Leu Glu Ile
50 55 60

Ser Ser Ile Phe Ser His Cys Cys Ser Leu Leu Ile Gly Val Val Ile
65 70 75 80

Gly Ser Ser Ser Lys Ile Lys Ala Glu Ala Glu Gln Ile Lys Lys Arg
85 90 95

Phe Lys Thr Met Met Ala Ala Val Asn Arg Pro Ser His Gly Glu Thr
100 105 110

Ala Thr Leu Leu Gln Met Phe Asn Pro His Glu Ala Ile Asp Trp Ile
115 120 125

Asn Gly Gln Pro Trp Val Gly Ser Phe Val Leu Ser Leu Leu Thr Thr
130 135 140

Asp Phe Glu Ser Pro Gly Lys Glu Phe Met Asp Gln Ile Lys Leu Val
145 150 155 160

Ala Ser Tyr Ala Gln Met Thr Thr Tyr Thr Thr Ile Lys Glu Tyr Leu
165 170 175

Ala Glu Cys Met Asp Ala Thr Leu Thr Ile Pro Val Val
180 185

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

His Thr Val Thr Pro Ser Leu Val Phe Leu Cys Leu Leu Ile Pro Gly
1 5 10 15

Leu His Ala Ala Phe Val His Gly Gly Val Pro Arg Glu Ser Tyr Leu
20 25 30

Ser Thr Pro Ile Thr Arg Gly Glu Gln Thr Val Val Lys Thr Ala Lys
35 40 45

Phe Tyr Gly Glu Lys Thr Thr Gln Arg Asp Leu Thr Glu Leu Glu Ile
50 55 60

Ser Ser Ile Phe Ser His Cys Cys Ser Leu Leu Ile Gly Val Val Ile
65 70 75 80

Gly Ser Ser Ser Lys Ile Lys Ala Gly Ala Glu Gln Ile Lys Lys Arg
85 90 95

Phe Lys Thr Met Met Ala Ala Leu Asn Arg Pro Ser His Gly Glu Thr
100 105 110

Ala Thr Leu Leu Gln Met Phe Asn Pro His Glu Ala Ile Asp Trp Ile
115 120 125

Asn Gly Gln Pro Trp Val Gly Ser Phe Val Leu Ser Leu Leu Thr Thr
130 135 140

Asp Phe Glu Ser Pro Gly Lys Glu Phe Met Asp Gln Ile Lys Leu Val
145 150 155 160

Ala Ser Tyr Ala Gln Met Thr Thr Tyr Thr Thr Ile Lys Glu Tyr Leu
165 170 175

Ala Glu Cys Met Asp Ala Thr Leu Thr Ile Pro Val Val
180 185

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Thr Met Ser Ser Thr Ala Leu Thr His Leu Leu Asn Arg Leu Ser His
1 5 10 15

Thr Ile Thr Lys Gly Asp Ser Phe Val Ile Asn Leu Asp Tyr Ser Ser
20 25 30

Trp Cys Asn Gly Phe Arg Pro Glu Leu Gln Ala Pro Ile Cys Arg Gln
35 40 45

Leu Asp Gln Met Phe Asn Cys Gly Tyr Phe Phe Arg Thr Gly Cys Thr
50 55 60

Leu Pro Cys Phe Thr Thr Phe Ile Ile Gln Asp Arg Phe Asn Pro Pro
65 70 75 80

Tyr Ser Leu Ser Gly Glu Pro Val Glu Asp Gly Val Thr Cys Ala Val
85 90 95

Gly Thr Lys Thr Met Gly Glu Gly Met Arg Gln Lys Leu Trp Thr Ile
100 105 110

Leu Thr Ser Cys Trp Glu Ile Ile Ala Leu Arg Glu Ile Asn Val Thr
115 120 125

Phe Asn Ile Leu Gly Gln Gly Asp Asn Gln Thr Ile Ile Ile His Lys
130 135 140

Ser Ala Ser Gln Asn Asn Gln Leu Leu Ala Glu Arg Ala Leu Gly Ala
145 150 155 160

Leu Tyr Lys His Ala Arg Leu Ala Gly His Asn Leu Lys Val Glu Glu
165 170 175

Cys Trp Val Ser Asp Cys Leu Tyr Glu Tyr Gly Lys Lys Leu Phe Phe
180 185 190

Arg Gly Val Pro Val Pro Gly Cys Leu Lys Gln Leu Ser Arg Val Thr
195 200 205

Asp Ser Thr Gly Glu Leu Phe Pro Asn Leu Tyr Ser Lys Leu Ala Cys
210 215 220

Leu Thr Ser Ser Cys
225

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ala Thr Gly Pro Ser Ser Leu Val Asp Ser Leu Glu Asp Glu Glu
1 5 10 15

Asp Pro

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Arg Ile Tyr Pro Gln Leu Pro Ser Ala Pro Thr Ala Asp Glu Trp Asp
1 5 10 15

Ile Ile Pro

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Asn Ser Lys His Ser Tyr Val Glu Leu Lys Gly Lys Val Ile Val
1 5 10 15

Pro Gly

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Arg Leu Arg Asn Ile Gly Val Gly Pro Leu Gly Pro Asp Ile Arg Ser
1 5 10 15

Ser Gly Pro

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Leu Ser Cys Asn Thr Asp Ser Thr Pro Gly Leu Ile Asp Leu Glu
1 5 10 15

Ile Arg

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Arg Ser Lys Leu Arg Arg Arg Arg Arg Asp Thr Gln Gln Ile Glu Tyr
1 5 10 15

Leu Val

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Leu Ile Ser Leu Cys Val Ser Leu Pro Ala Ser Phe Ala Arg Arg Arg
1 5 10 15

Arg Leu Gly Arg Trp Gln Glu
20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Pro Pro Lys Arg Arg Leu Val Asp Asp Ala Asp Ala Met Glu Asp
1 5 10 15

Gln Asp

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Glu Asp Gln Asp Asp Leu Tyr Glu Pro Pro Ala Ser Leu Pro Lys
1 5 10 15

Leu Pro

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Glu Leu Ser Gly Glu Ile Ser Ala Ile Met Arg Met Ile Gly Val Thr
1 5 10 15

Gly Leu Val

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CAGGAGGCTC AATGGCAACG 20

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTTATGGTAT GATGTCCCAC 20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATCGAATCAC CATGAATTCA AAGC 24

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GTCAGTATTG CAACTAAGGC 20

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GCACGCAATT AATGCAGC 18

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CAGTGTAGGC CTAAGCTTGT G 21

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAGTTGAGAA GGCGGCGTAG 20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGGTACGGTT TATTCCTGC 19

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGACCATGAG CTCAACGGC 19

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GCATGATGAT GTTAAGCAGG C 21

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TTCATACAGT AACGCCCAGC 20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GCAACTACAG GGATTGTAAG GG 22

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCCTTGTGTT TCTATGTTTG C 21

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCATCCATAC ATTCTGCGAG 20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CGAATTCGCA CGCAATTAAT GCAGC 25

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GCTACTCGAG CGGTACGGTT TATTCCTGC 29

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CCCCCCGGGC AATGTACTGC AGTTTCGCGG ACT 33

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGGCCCGGGT TATTCCTGCC ACCGGCCGA 29

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATGCCACCCG GGAGACGCCT GATTGAT 27

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGGATCCCGG GCTAGTTTAG ACCAGTCACT CC 32

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GGCCATATGC GCCCGGGCCC ATCGAGTCTG GTCGACTCCC TG 42

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CTCGAGCCCG GGTTATGGTA TGATGTCCCA CTCATC 36

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CGAATCCCCG GGAATTCAAA GCATTCCTA 29

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCCCCCCGGG CAGTATTGCA ACTAACGG 28

What is claimed is:

1. A substantially purified nucleic acid encoding a human Borna disease virus (BDV) p24 polypeptide comprising an amino acid residue sequence selected from the group consisting of SEQ ID NO 20, SEQ ID NO 21, SEQ ID NO 22, MATGPSSLVDSLEDEEDP (SEQ ID NO 32) and RIYPQLPSAPTADEWDIIP (SEQ ID NO 33).

2. The nucleic acid according to claim 1 wherein the nucleic acid consists essentially of a nucleotide sequence of SEQ ID NO 3.

3. The nucleic acid according to claim 1 wherein the nucleic acid consists essentially of a nucleotide sequence of SEQ ID NO 4.

4. The nucleic acid according to claim 1 wherein the nucleic acid consists essentially of a nucleotide sequence of SEQ ID NO 5.

5. A substantially purified nucleic acid encoding a human Borna disease virus (BDV) p16 polypeptide comprising an amino acid residue sequence selected from the group consisting of SEQ ID NO 23, SEQ ID NO 24, SEQ ID NO 25, MNSKHSYVELKGKVIVPG (SEQ ID NO 34) and RLRNIGVGPLGPDIRSSGP (SEQ ID NO 35).

6. The nucleic acid according to claim 5 wherein the nucleic acid consists essentially of a nucleotide sequence of SEQ ID NO 7.

7. The nucleic acid according to claim 5 wherein the nucleic acid consists essentially of a nucleotide sequence of SEQ ID NO 8.

8. The nucleic acid according to claim 5 wherein the nucleic acid consists essentially of a nucleotide sequence of SEQ ID NO 9.

9. A substantially purified nucleic acid encoding a human Borna disease virus (BDV) p56 polypeptide comprising an amino acid residue sequence selected from the group consisting of SEQ ID NO 26, SEQ ID NO 27, GLSCNTDSTPGLIDLEIR (SEQ ID NO 36), RSKLRRRRRDTQQIEYLV (SEQ ID NO 37) and LISLCVSLPASFARRRRLGRWQE (SEQ ID NO 38).

10. The nucleic acid according to claim 9 wherein the nucleic acid consists essentially of a nucleotide sequence of SEQ ID NO 11.

11. The nucleic acid according to claim 9 wherein the nucleic acid consists essentially of a nucleotide sequence of SEQ ID NO 12.

12. A substantially purified nucleic acid encoding a human Borna disease virus (BDV) p40 polypeptide consisting essentially of an amino acid residue sequence selected from the group consisting of SEQ ID NO 28, SEQ ID NO 29, SEQ ID NO 30, MPPKRRLVDDADAMEDQD (SEQ ID NO 39), MEDQDDLYEPPASLPKLP (SEQ ID NO 40) and ELSGEISAIMRMIGVTGLN (SEQ ID NO 41).

13. The nucleic acid according to claim 12 wherein the nucleic acid consists of a nucleotide sequence of SEQ ID NO 14.

14. The nucleic acid according to claim 12 wherein the nucleic acid consists of a nucleotide sequence of SEQ ID NO 15.

15. The nucleic acid according to claim 12 wherein the nucleic acid consists of a nucleotide sequence of SEQ ID NO 16.

16. A substantially purified nucleic acid encoding a human Borna disease virus (BDV) catalytic domain polypeptide of L polymerase protein consisting essentially of an amino acid residue sequence in SEQ ID NO 31.

17. The nucleic acid according to claim 16 wherein the nucleic acid consists of a nucleotide sequence of SEQ ID NO 18.

18. The nucleic acid according to claim 16 wherein the nucleic acid consists of a nucleotide sequence of SEQ ID NO 19.

19. A vector containing a nucleic acid of claim 1.

20. The vector according to claim 19 wherein the vector is an expression vector and the nucleic acid is operably linked to a promoter.

21. The vector according to claim 20 wherein the nucleic acid consists of a nucleotide sequence of claims 2, 3 or 4.

22. A vector containing a nucleic acid of claim 5.

23. The vector according to claim 22 wherein the vector is an expression vector and the nucleic acid is operably linked to a promoter.

24. The vector according to claim 23 wherein the nucleic acid consists of a nucleotide sequence of claims 6, 7 or 8.

25. A vector containing a nucleic acid of claim 9.

26. The vector according to claim 25 wherein the vector is an expression vector and the nucleic acid is operably linked to a promoter.

27. The vector according to claim 26 wherein the nucleic acid consists of a nucleotide sequence of claims 10 or 11.

28. A vector containing a nucleic acid of claim 12.

29. The vector according to claim 28 wherein the vector is an expression vector and the nucleic acid is operably linked to a promoter.

30. The vector according to claim 29 wherein the nucleic acid consists of a nucleotide sequence of claims 13, 14 or 15.

31. A vector containing a nucleic acid of claim 16.

32. The vector according to claim 31 wherein the vector is an expression vector and the nucleic acid is operably linked to a promoter.

33. The vector according to claim 32 wherein the nucleic acid consists of a nucleotide sequence of claims 17 or 18.

34. A cell transformed with the expression vector of claims 20, 23, 26, 29 or 32.

35. A substantially purified polypeptide corresponding to human Borna disease virus (BDV) p24 polypeptide comprising an amino acid residue sequence selected from the group consisting of SEQ ID NO 20, SEQ ID NO 21, SEQ ID NO 22, MATGPSSLVDSLEDEEDP (SEQ ID NO 32) and RIYPQLPSAPTADEWDIIP (SEQ ID NO 33).

36. The polypeptide according to claim 35 wherein the polypeptide is a synthetic polypeptide.

37. The polypeptide according to claim 35 wherein the polypeptide is a recombinant polypeptide.

38. The polypeptide according to claim 37 wherein the recombinant polypeptide is a fusion protein.

39. A substantially purified polypeptide corresponding to human Borna disease virus (BDV) p16 polypeptide consisting essentially of an amino acid residue sequence selected from the group consisting of SEQ ID NO 23, SEQ ID NO 24, SEQ ID NO 25, MNSKHSYVELKGKVIVPG (SEQ ID NO 34) and RLRNIGVGPLGPDIRSSGP (SEQ ID NO 35).

40. The polypeptide according to claim 39 wherein the polypeptide is a synthetic polypeptide.

41. The polypeptide according to claim 39 wherein the polypeptide is a recombinant polypeptide.

42. The polypeptide according to claim 41 wherein the recombinant polypeptide is a fusion protein.

43. A substantially purified polypeptide corresponding to human Borna disease virus (BDV) p56 polypeptide consisting essentially of an amino acid residue sequence selected from the group consisting of SEQ ID NO 26, SEQ ID NO 27, GLSCNTDSTPGLIDLEIR (SEQ ID NO 36), RSKLRRRRRDTQQIEYLV (SEQ ID NO 37) and LISLCVSLPASFARRRRLGRWQE (SEQ ID NO 38).

44. The polypeptide according to claim 43 wherein the polypeptide is a synthetic polypeptide.

45. The polypeptide according to claim 43 wherein the polypeptide is a recombinant polypeptide.

46. The polypeptide according to claim 45 wherein the recombinant polypeptide is a fusion protein.

47. A substantially purified polypeptide corresponding to human Borna disease virus (BDV) p40 polypeptide comprising an amino acid residue sequence selected from the group consisting of SEQ ID NO 28, SEQ ID NO 29, SEQ ID NO 30, MPPKRRLVDDADAMEDQD (SEQ ID NO 39), MEDQDDLYEPPASLPKLP (SEQ ID NO 40) and ELSGEISAIMRMIGVTGLN (SEQ ID NO 41).

48. The polypeptide according to claim 47 wherein the polypeptide is a synthetic polypeptide.

49. The polypeptide according to claim 47 wherein the polypeptide is a recombinant polypeptide.

50. The polypeptide according to claim 49 wherein the recombinant polypeptide is a fusion protein.

51. A substantially purified polypeptide corresponding to human Borna disease virus (BDV) catalytic domain polypeptide of L polymerase protein consisting essentially of an amino acid residue sequence in SEQ ID NO 31.

52. The polypeptide according to claim 51 wherein the polypeptide is a synthetic polypeptide.

53. The polypeptide according to claim 51 wherein the polypeptide is a recombinant polypeptide.

54. The polypeptide according to claim 53 wherein the recombinant polypeptide is a fusion protein.

55. An anti-human BDV p24 polypeptide antibody comprising antibody molecules that immunoreact with human BDV and a polypeptide of claim 35.

56. An anti-human BDV p16 polypeptide antibody comprising antibody molecules that immunoreact with human BDV and a polypeptide of claim 39.

57. An anti-human BDV p56 polypeptide antibody comprising antibody molecules that immunoreact with human BDV and a polypeptide of claim 43.

58. An anti-human BDV p40 polypeptide antibody comprising antibody molecules that immunoreact with human BDV and a polypeptide of claim 47.

59. An anti-human BDV catalytic domain polypeptide antibody comprising antibody molecules that immunoreact with human BDV and a polypeptide of claim 51.

60. A method of detecting a BDV nucleic acid in a sample, the method comprising hybridizing the nucleic acid in the sample with a nucleic acid of claims 1, 5, 9, 12 or 16.

61. The method according to claim 60 wherein the sample is a BDV-infectable cell.

62. The method according to claim 61 wherein the cell is a peripheral blood mononuclear cell.

63. The method according to claim 60 wherein the sample is isolated from a human.

64. The method according to claim 60 wherein detecting the BDV nucleic acid is for diagnosing BDV infection.

65. The method according to claim 64 wherein the infection is in a subject having a neuropsychiatric disorder.

66. A method for detecting a BDV ligand in a sample, the method comprising the steps of:

(a) contacting the sample with a human BDV polypeptide of claims 35, 39, 43, 47 or 51 for a time period

sufficient to allow the polypeptide to immunoreact with the BDV ligand thereby forming an immunoreaction complex; and

(b) detecting the immunoreaction complex.

67. The method according to claim 66 wherein the BDV ligand is an antibody.

68. The method according to claim 66 wherein the immunoreaction complex is detected by the addition of a detecting antibody that binds to the immunoreaction complex.

69. The method according to claim 66 wherein the immunoreaction complex is detected by the indirect immunofluorescence focus assay.

70. The method according to claim 68 wherein the detecting antibody contains a label.

71. The method according to claim 70 wherein the label is selected from the group consisting of enzymes, radioisotopes, fluorescent compounds, colloidal metals, chemiluminescent compounds, phosphorescent compounds and bioluminescent compounds.

72. The method according to claim 66 wherein the polypeptide is immobilized on a solid support.

73. The method according to claim 66 wherein the sample comprises a body fluid.

74. The method according to claim 73 wherein the body fluid is serum.

75. The method according to claim 66 wherein the sample is isolated from a human.

76. The method according to claim 66 wherein detecting the BDV ligand is for diagnosing BDV infection.

77. The method according to claim 76 wherein the infection is in a subject having a neuropsychiatric disorder.

78. A method for detecting a BDV antigen in a sample, the method comprising the steps of:

(a) contacting the sample with an anti-human BDV antibody of claims 55, 56, 57, 58 or 59 for a time period sufficient to allow the antibody to immunoreact with the BDV antigen present in the sample thereby forming an immunoreaction complex; and

(b) detecting the immunoreaction complex.

79. The method according to claim 78 wherein the immunoreaction complex of said step (b) is detected by the addition of a detecting antibody.

80. The method according to claim 79 wherein the detecting antibody contains a label.

81. The method according to claim 80 wherein the label is selected from the group consisting of enzymes, radioisotopes, fluorescent compounds, colloidal metals, chemiluminescent compounds, phosphorescent compounds and bioluminescent compounds.

82. The method according to claim 78 wherein the anti-human BDV antibody is immobilized on a solid support.

83. The method according to claim 78 wherein the sample comprises cells.

84. The method according to claim 83 wherein the cells are peripheral blood mononuclear cells.

85. The method according to claim 78 wherein the immunoreaction complex of said step (b) is detected by flow cytometry.

86. The method according to claim 78 wherein the immunoreaction complex of said step (b) is detected by ELISA.

87. The method according to claim 78 wherein the immunoreaction complex of said step (b) is detected by immunoblot analysis.

88. A kit for detecting the presence of BDV nucleic acid in a sample, the kit comprising packaging means being compartmentalized to receive in close confinement therein one or more containers comprising separate containers containing a human BDV nucleic acid of claims 1, 5, 9, 12 or 16.

89. A kit for detecting the presence of a BDV antibody in a sample, the kit comprising packaging means being compartmentalized to receive in close confinement therein one or more containers comprising a first container containing a polypeptide of claims 35, 39, 43, 47 or 51.

90. The kit according to claim 89 further comprising a second container containing a detecting antibody.

91. The kit according to claim 90 wherein the detecting antibody contains a label.

92. The kit according to claim 91 wherein the label is selected from the group consisting of enzymes, radioisotopes, fluorescent compounds, colloidal metals, chemiluminescent compounds, phosphorescent compounds and bioluminescent compounds.

93. The kit according to claim 89 wherein the polypeptide is immobilized on a solid support.

94. A kit for detecting a BDV antigen in a sample, the kit comprising packaging means being compartmentalized to receive in close confinement therein one or more containers

comprising a first container containing an anti-human BDV polypeptide antibody of claims 55, 56, 57, 58 or 59.

95. The kit according to claim 94 further comprising a second container containing a detecting antibody.

96. The kit according to claim 95 wherein the detecting antibody contains a label.

97. The kit according to claim 96 wherein the label is selected from the group consisting of enzymes, radioisotopes, fluorescent compounds, colloidal metals, chemiluminescent compounds, phosphorescent compounds and bioluminescent compounds.